

T D D E T T F G S S G G G G

10 50
GTTTGGCTCTGGCAAGCTGGCATATTGGAAAGCTTTTCCGGCTCTGGAGGGGT-29
-88 70 90 110 31
CCTGCTTCTTCCCTACAGCCGTTCCGGGCATGGCTGGGGCTGGCTCCACGTCT
M A W L G A S L H V W 11
-8 130 150 170 91 31
GGGGTTGGCTAATGGCTCGGCAGCTGGCTCCCTGGCCAGAGCCCAGCTGGATTCTGATGGCA
G W L M L G S C L A R A Q L D S D G T
12 190 210 230 151 51
CCATCACTATAAGGGAGGAGATTGGCTCTGGCTGAAAGCAGAACATGTGAACCTCA
I T I E E Q I V L V L K A K V Q C E L N
32 250 270 290 211 71
ACATCACAGCTCAA CCAACTCCAGGGAGGAAGGTAATTGGTTCCCTGAATGGGATGGACTCA
I T A Q L Q E G N C F P E W D G L I
52 310 330 350 271 91
TTTGGGGCCAGAGGAACAGTGGGGAAAATATCGGCTGTTCCATGCCCTCCCTTATTT
C W P R G T V G K I S A V P C P Y I Y
72 370 390 410 331 111
ATGACTTCAACCATAAGGGAGTTGGCTGACACTGTAACCCCCAATGGAAACATGGGATT
D F N H K G V A F R H C N P N G T W D F
92 MATCH WITH FIG. 1B

FIG. 1A

MATCH WITH FIG. 1A

332	TTATGCACAGCTTAATAAACATGGGCCAATT	430	CAGACTGCTTCTGCTTTCTGCAGGC	470	GCCTTGCTTTCTGCAGGC	391
112	M H S L N K T W A N Y S D C L R F L Q P					131
392	CAGATATCAGCATAGGAAAGCAAGAAATT	490	TGTGAACGCCCTCTATGTAATACCGTTG	530	TGTGAACGCCCTCTATGTAATACCGTTG	451
132	D I S T G K Q E F C E R L Y V M Y T V G					151
452	GCTACTCCATCTCTTTGGCTTCTGGCTTCTGGCTTCTGGCTTACTTCAGAC	550	GCTACTCCATCTCTGGCTTCTGGCTTACTTCAGAC	590	GCTACTCCATCTCTGGCTTACTTCAGAC	511
152	Y S I S F G S L A V A I L I I G Y F R R					171
512	GATTGCATTGCACTTATCCACATGGACTTATTGTGTCTTCATGCTGAGAG	610	GATTGCATTGCACTTATCCACATGGACTTATTGTGTCTTCATGCTGAGAG	650	GATTGCATTGCACTTATCCACATGGACTTATTGTGTCTTCATGCTGAGAG	571
172	L H C T R N Y I H M H L F V S F M L R A					191
572	CTACAAGCATCTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAGGGAGCTGG	670	CTACAAGCATCTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAGGGAGCTGG	710	CTACAAGCATCTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAGGGAGCTGG	631
192	T S I F V K D R V V H A H I G V K E L E					211
632	AGTCCCTAATAATGCAGGATGACCCACAAATTCCATTGAGGCAACTCTGTGGACAAAT	730	AGTCCCTAATAATGCAGGATGACCCACAAATTCCATTGAGGCAACTCTGTGGACAAAT	770	AGTCCCTAATAATGCAGGATGACCCACAAATTCCATTGAGGCAACTCTGTGGACAAAT	691
212	S L I M Q D P Q N S I E A T S V D K S					231
		790	810	830		
					MATCH WITH FIG. 1C	

FIG. 1B

Y D D E T T T A G G S G G F S D

MATCH WITH FIG. 1B

692	ACAATATATGGGTGCAAGATTGGTGTGATGTTTACTTCCTGGCTACAAATT	751
232	Q Y I G C K I A V V M F I Y F L A T N Y	251
850	870	890
752	ATTATTGGATCCTGGGAAGGGTCTACCTGCATAATCTCATCTGGCTTCTTT	811
252	Y W I L V E G L Y L H N L I F V A F F S	271
910	930	950
812	CGGACACAAATAACCTGTGGGCTTCATCTGATAAGGGCTGGGGTTCCAGCAGCATTG	871
272	D T K Y L W G F I L I G W G F P A A F V	291
970	990	1010
872	TTGCAGCATGGCTGTGGCACGAGCAACTCTGGCTGATGGAGGTGGAACTTAGTG	931
292	A A W A V A R A T L A D A R C W E L S A	311
1030	1050	1070
932	CTGGAGACATCAAGTGGATTATCAAGCACCGATCTTAGCAGCTATTGGCTGAATTTA	991
312	G D I K W T Y Q A P I L A I G L N F I	331
1090	1110	1130
992	TTCTGTTCTGAATAACGGTTAGAGTTCTAGCTACCAAAATCTGGAGACCAATGGAGTTG	1051
332	L F L N T V R V L A T K I W E T N A V G	351
1150	1170	1190
1052	GGCATGACACAAGGAAGCAAATACAGGAAACTGGCCAAATCGACACTGGTCTGGCTAG	1111
352	H D T R K Q Y R K L A K S T L V L V	371

FIG. 1C

MATCH WITH FIG. 1C

1112	TCTTTGGAGTCATTACATCGTGTGCTGCCTCACTCCCTGACTGGGCTGGGT	1171
372	F G V H Y I V F V C L P H S F T G L G W	391
1210	1230	1250
1172	GGGAGATCCGCATGCACTGTGAGCTCTTCAACTCCCTTCAGGGTTCTTGTGAGTCCTA	1231
392	E I R M H C E L F F N S F Q G F V S I	411
1270	1290	1310
1232	TCATCTACTGCTACTGCAAATGGAGAGGTTCAAGGAGGGTGAAGAAGATGTGGAGTCGGT	1291
412	I Y C Y C N G E V Q A E V K M W S R W	431
1330	1350	1370
1292	GGAATCTCTCCGTGGACTGGAAAGGACACCCCATGTGGCAGCCAGATGGGCTCAG	1351
432	N L S V D W K R T P P C G S R R C G S V	451
1390	1410	1430
1450	1470	1490
1352	TGCTCACCCACCGTGACGCCACAGCACAGGCAAGTCACAGGTGGCGCAGCACACGGAT	1411
452	L T T V T H S T S Q S Q V A A H A W	471
1510	1530	1550
1412	GGTGCCTATCTCTGGCAAAAGCTGCCAAGATGCCAGGACAGCAGCTGACAGGCCACATCAC	1471
472	C L S L A K L P R S P A D S L T A T S L	491

MATCH WITH FIG. 1E

FIG.1D

MATCH WITH FIG. 1D

1472	TTTACCTGGCTATGAGTAACCTAGAGCAGGA 492 Y L A M S G V T Q S R T A S H	1570 1590 1610	CACACTCTCCACAGA T L S T R 511
1532	GGAGCAACAAGGAAGATAAGTGGAGGCAGAGA 512 S N K E D S G R Q R D D I L M E	1630 1650 1670	TAATGGAGAAGGCCCTCCA P S R 531
1592	GGCCTATGGAATCTAACCCAGACACTGAAGGG 532 P M E S N P D T E G	1690 1710 1730	TCAAGGAAACTGAGGATGTCTCT 541
1652	GAATGGACATGTTGGCTGACTTTCATGGCTGG 1750 CAATGGCTTAAAGGCTGAGCACAAGG 1712 GATACTCCTATGCTTGAAATTCAAGGTGG 1790 GC 1711	1750 1770 1790	TGTGAGAGGGC
1772	TAATAGTTTTAGGCTCCATGAATTGGCTCCTG 1870 TAATACCTATGCTGAAATACTAACGACAT 1771	1810 1830 1850	GAAATGCAAG 1771
1832	TGTCAATGGAGTAGTTTATTACCTTCATGGCA 1892 TCAAGGTGTTCTAAATTAAATGTAT 1990 GTATTGGCTCTGTGATTGTTCA	1930 1950 1970	1831 1891 1914

FIG. 1E

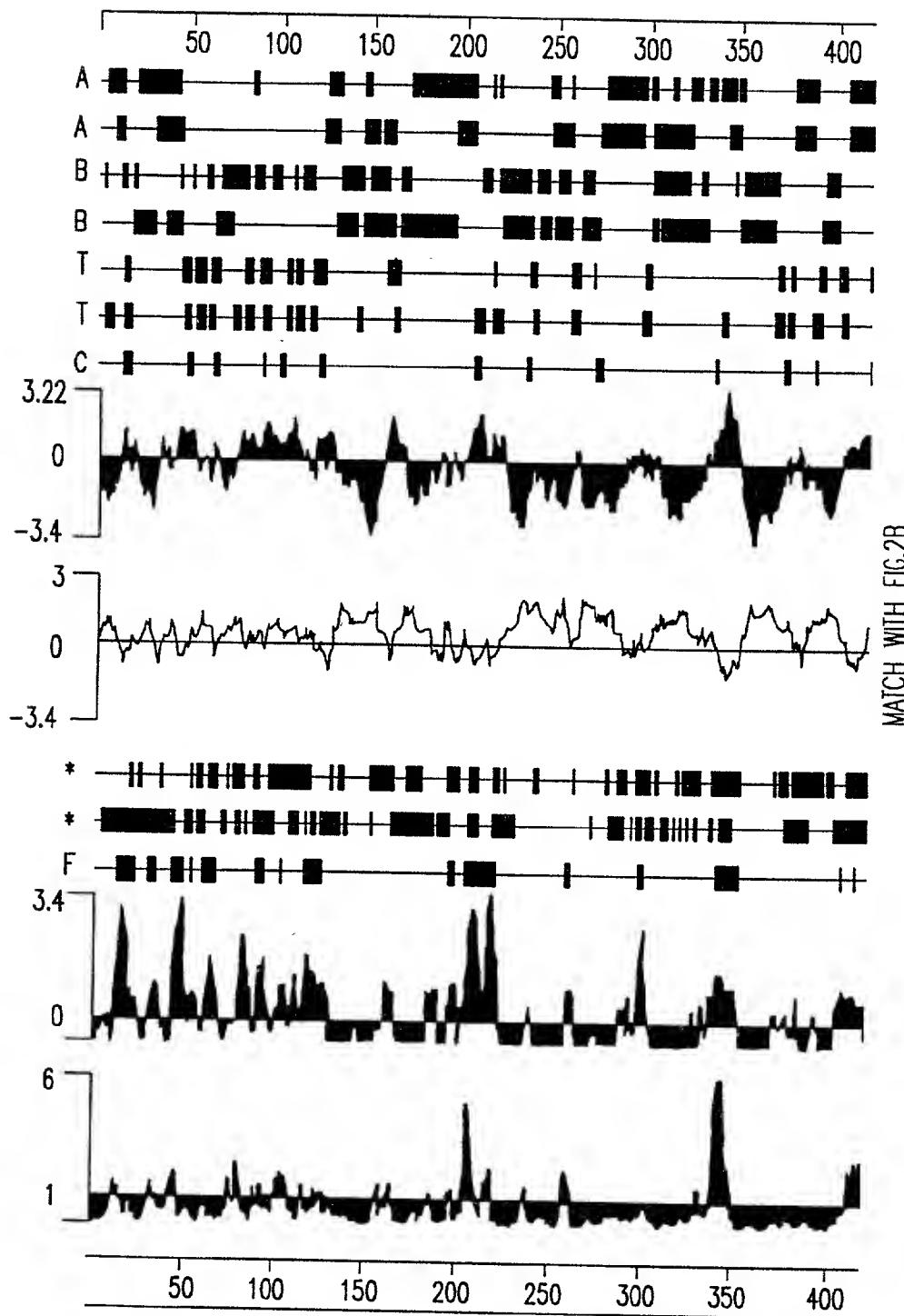


FIG. 2A

450 500

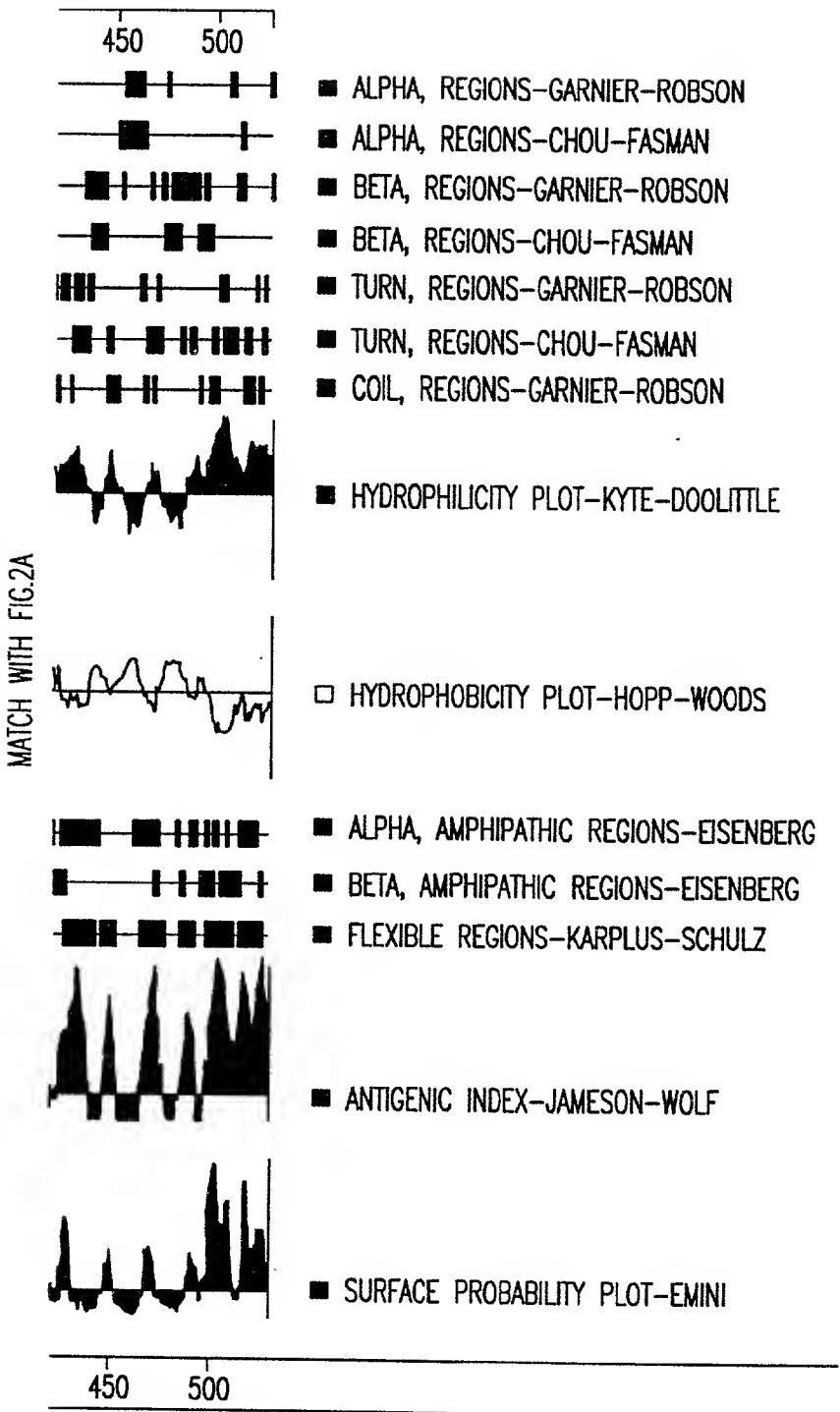


FIG. 2B

Sequences producing high-scoring Segment Pairs:	Reading Frame	High Score	P(N)	Probability N
gp M74445 OPOPTHR_1	parathyroid hormone receptor [Di...]	+3	597	8.2e-204
pir S A39286	parathyroid hormone / parathyroid...	+3	597	2.9e-203
gp L04308 HUMPTHR_1	parathyroid hormone receptor [Ho...]	+3	580	6.7e-190
pir S S29610	parathyroid hormone receptor - h...	+3	580	6.1e-189
gp M77184 RATPATHYR_1	parathyroid hormone receptor [Ra...]	+3	576	7.7e-188
gp X78936 IMMPHRPR_1	parathyroid hormone/parathyroid ...	+3	576	7.7e-188
pir S A42698	parathyroid hormone and parathyry...	+3	576	7.7e-188
gp L34611 MUSPTHR06_1	parathyroid hormone/parathyroid ...	+3	576	4.1e-174
gp U11087 HSV1RG9_1	vasoactive intestinal peptide 1 ...	+3	319	1.2e-98
gp M86835 RATVASREC_1	vasoactive intestinal polypeptid...	+3	254	3.1e-91

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|M74445|OPOPTHR_1 parathyroid hormone receptor [Didelphis virginiana]
Length = 585

Plus Strand HSPs:

score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Match with FIG. 3B

FIG. 3A

Match with FIG. 3 A

Query: 729 IMODDPONSIPEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDT 908
 I +++ + E DK+ ++GC++AV +F+YFL TNYYWILVEGLYLH+LIF+AFFS+
 Sbjct: 253 ITEEEELRAFTTEPPPADKAGETVGCRVAVTVFPLYFLTTNYWILVEGLYLHSLIFMAFFSEK 312

Query: 909 KYLWGFFILLIGWGF FAAFVAAWAVARATLADARCWELSAGDIRWYQAPILLAIGLNFILE 1088
 KYLWGFF L GWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFILF
 Sbjct: 313 KYLWGFTLFGWGLPAVFTVAVWNTVRATLANTECWDLSSGNKKWIIQVPIILAATVVNFILE 372

Query: 1089 LNTVRVLATKWIETNAVGHDTRKQYRKLAKSTLVLVILVEGVHYIVFVCLPHS 1244
 +N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++
 Sbjct: 373 INIIRVLATKLIRETNAGRCDTRQQYRKLLRKSTLVLMPLEFGVHYIVFMATPYT 424

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPEWNDGLICWPRGTVKGKISAVPCPPYIYDFNHKGVAFRHICNPNGTWDFMHSLNKTW 446
 +G C PEWD ++CWP G GK+ AVPCP YIYDFNHKG A+R C+ NG+W+ + N+TW
 Sbjct: 102 DGFCLPWENDNIVCWPAGVPGKVVAWPCPDYIYDFNHKGRAYRRCDSNGSWELLVPGNINRTW 161

Query: 447 ANYSDCLRFL 476
 ANYS+C++FL

Sbjct: 162 ANYSECVKFL 171

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRRLHCTRNYIHMHLFVSFMLRATSIFV 677
 ++E +RL ++YTVGYSIS GSL VA+LI+GYFRRRLHCTRNYIHMHLFVSFMLRA SIF+

FIG. 3B

MATCH WITH FIG. 3B
sbjct: 177 EREVFDRLGMIYTVGYSISLGSLLTAVLILGYFRRLHCTRNYIHMHLFVSEMLRAVSIFI 236

Query: 678 KDRVVAHTIGVKELESLIMOD 740
 KD V+++ + E+E + ++
sbjct: 237 KDAVLYSGVSTDETERITEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFNSFQGFFFSIIYCYCNGEVQAEVKMWRSWNLSTVDMKRTTPPCGS 1424
 +G+ W+++MH E+ FNSFQGFFV+IIYC+CNGEVQAE+KK WSRW L+D+KR GS
sbjct: 427 SGILMQVQMHYEMLFNSFQGFFFVALLYCFCCNGEVQAEIKKSWSRWTLALDFKRKARSGS 485

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query: 159 AQLIDSDGTITIEEQITVLVAKVQCELNITAQLQEGER 269
 A +D+D IT EEQI+L+ A+ QCE + L+ E
sbjct: 24 ALVDADDVITKEEQIILLRNAQAQCEQRILKEVLRVPE 60

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISGKAAKIASRQPDSHTILPGYV 1576
 +S + A A + H LPGYV
sbjct: 512 LSPRLAPGAGASANGHHQLPGYV 534

FIG. 3C